

SEQUENCE LISTING

<110> NELSON, DAVID R.

<120> A LIVE, AVIRULENT STRAIN OF V. ANGUILLARUM THAT
PROTECTS FISH AGAINST INFECTION BY VIRULENT V.
ANGUILLARUM

<130> 5112

<140>

<141>

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 3609

<212> DNA

<213> V. Anguillarum.

<220>

<223> "n" bases may be a, t, c, g, other or unknown

<400> 1

```

gtcgacttat tgcattgatg gcgtacatgg tagtgccatc cttcgtttgc taacaagcgt 60
tgtataaaaag cttggtcggt ttcacacaaat actcatgatt tttcccactt 120
ccggaaaggg aaaagtgaag atagcttttg agatcagcct gttctagcag cttttcaatg 180
atctttttcg tcgttacggt ttgaaaaatc tgacgactgc gtttgatttg caacaagcta 240
agtggatcca atatctctat ttgataataa aactgctgct tgtctttgct ataccctgtg 300
aattgcagag tgctacatat acctgaaaaa aaacgctttc cagaatctaa ttcgtaagac 360
acacaaacag ctttacctag gtttttggtt tcgactctca tgtttgccgc gatggaaacg 420
gaaaactgac acccgccgga tacgcttttc tctccgatta attgcgtgac aatataactt 480
ttgctatctg aaagcttaat ggtgaggagg cgggtttggt gctttaattc gttactgctc 540
atattcaatt aattcactat taaataaaca gttctaaaag gctgtttatt ggatgaatat 600
tcgaaattat cacataataa ttgatgctat tattacttgc tgtattggtt tcaactttca 660
tgctctatac atgtaataa tttcgagtta gaccttaatt caaggtaatt tgtctattta 720
attattatct gaataatatg taatcgattg ctttgtgggt atttttatgt ttgtttcatt 780
tttaatgacg gtgagcttgt gcattcatat tttttatgat gacaacatct ttgatgaagt 840
atttaagata ttgttaatgc atgaggggtt tgcgtgtatt ttttatatta aatcataata 900
aatcaacaa tatatgttat tttgtgtcct tttatagtgt tcttttaaag aggtaggatg 960
acctaaaggt cgcctagaaa tatggcgtta attgccattg ctataattca cctcaaagat 1020
acactattgg caaattgaca aatatgtcac ttcgtatgaa acaatattag tagatgttgt 1080
ttttgctgca aaaataaaaa tttttctggt tgaaataact caaggcctct agcgttttcc 1140
tttatcttaa aatacaggaa atagcgattg aagttaattg aactttaagc aasdramgaa 1200
tagtcaacct aacagagcag gaacctatgc ctttgtcaaa gcatcaaatt gagcaacttt 1260
ctaaacctct gagtgatgat tcgatctgtg gcgtttatct taaactggaa aaaagtgtct 1320
ttcgccattt acgtaatgaa tttaatgtcg cgcaactgct gctgcgtaag ctaagtcaaa 1380
acctagtgc tgacgagaga gatgcgttac aagaggcatg tctaaataag tggaagattc 1440
tctctgacag tttgtacgaa cagttttcaa aaacaaccag agatctcgag ctcatctcat 1500
ggtttggtgc tgctcaattc cttctcgata ccacattaga aagtgtgctg aatagccttg 1560
agtggttagc ggatttaagt gagaagcact gggatcacct caaccctgta ctaccagttg 1620
aaacgctcaa atctgatgat gataagggca aagaaagaga gcaagcagat gcgaaagtta 1680
aagcattttt ccaactagtc ggcgatagcg aggaaagctc gattctctat gcgcccgtgc 1740
tgcaactgcc cttagtcggg gaagtgcggt tttttgactt tcaaagtgcg gagagaaaag 1800
gcgaaatcag ccaactgaaa tctatgctta cgaccacggt ggcgcaagag cgtttcgcaa 1860
ttcaattcaa gatggaaaac gccaaacggt gtgtcaccca attagatcgt ttgtcagcgt 1920

```

tgggtgagcac taagtgtcat tctctaggca gtcaaagtac caacttcgga tttgcgaagt 1980
 cactgcttac ccggtgttgaa aacgctttgg ttcattctaag tggaattaaag ttagcaccga 2040
 aagcggaggc caagacagta gagcaagagg ttgccgaaag ttcagtttct gaaggggagc 2100
 tgccaagcca tatggatata aaacatatag agcgaatacc gatggcatca gagcaggctc 2160
 agaccgtaag ccaacactta cacgcaggaa acctctctga actgggtaat ttaaacaata 2220
 tgaaccgaga cttagctttc catttggtga gagaagtctc tgattatatt cgccagagcg 2280
 aaccgcatag cccaatttca tttttgtag aaaaagcgat tcgatgggga tatttatcct 2340
 tacctgagtt gctgcgagaa atgatgtcgg aacaaaacgg tgacgctctt agtacgattt 2400
 ttaatgccgc cggattgaat catctcgatc aggttttgct gccggagggt agtactccaa 2460
 cgggtgggcat tgaaagcccc caaacacctc aagcgaagcc ttccgtttcg gatccgcgaa 2520
 gtgttgaaga gcatgtatct cagacttccc ctgtagatac ccaatctaag caagatcaaa 2580
 aaccacaatc atccgcta*s drbcgtcggc tctgagttgg taattgtgtt taaaaaataa 2640
 ggaaaaatca tggcaagtat ttacatgcgt gtaagcggtc ttcaagttga gggcgcagcg 2700
 actatcgggc agctagaaac ggctgaagg aaaaatgacg gttggtttgc aatcaactct 2760
 tactcttggg gtggcgctcg taacgttgct atggacatcg gtaacggcac caatgcggat 2820
 tcaggcatgg ttggcgtaag cgaagttagc gtaactaaag aagtcgatgg tgcttctgaa 2880
 gacctactgt cttattttatt caaccagggt aaagacggta aaactggtga ggttgcat 2940
 actaagcctt ctaacgatgg tcaaggtgca gacgtttact tccaagttaa gctagaaaaa 3000
 gcacgtttag tttcttataa cgtgagcggg actgacggat ctcaaccgta cgagagccta 3060
 tctctttctt acacttctat ttctcagaag catcactatg agaaagaagg tgggtgaacta 3120
 caaagcgggt gtgttgtgac ttacgaccta ccgaccggga aaa*tgactt ctggttaagta 3180
 attctttcat tagacatgcc acgttaattg gcatgtctat ttcatgaata tctcsdrcat 3240
 tttaggacac cgttatggca ttgaactcac aacataagcg cgtagtaag aaccgtgtca 3300
 gcatcaccta tgacgttgaa acgaatggcg ccgtaaagac gaaagagctg ccgtttgttg 3360
 ttggcgctcat tggcgacttt tcaggacaca aaccagaatc agaaaaagtt gatttagaag 3420
 agcgagagtt cacgggtatc gataaagaca acttcgatac agtgatgggg caaattcacc 3480
 cgcgtctttc gtacaagggt gataacaagc ttgctaata tgatagccag tttgaagtga 3540
 acttgagcct ccgttcgatg aaagatttcc acccagagaa cttagttgat naaattgagc 3600
 cgcttaaag 3609

<210> 2

<211> 463

<212> PRT

<213> V. Anguillarum

<400> 2

Met	Pro	Leu	Ser	Lys	His	Gln	Ile	Glu	Gln	Leu	Ser	Lys	Pro	Leu	Ser
1				5					10					15	
Asp	Asp	Ser	Ile	Cys	Gly	Val	Tyr	Leu	Lys	Leu	Glu	Lys	Ser	Ala	Phe
			20					25					30		
Arg	Pro	Leu	Arg	Asn	Glu	Phe	Asn	Val	Ala	Gln	Thr	Ala	Leu	Arg	Lys
		35					40					45			
Leu	Ser	Gln	Asn	Pro	Ser	Ala	Asp	Glu	Arg	Asp	Ala	Leu	Gln	Glu	Ala
	50					55					60				
Cys	Leu	Asn	Lys	Trp	Lys	Ile	Leu	Ser	Asp	Ser	Leu	Tyr	Glu	Gln	Phe
65					70					75					80
Ser	Lys	Thr	Thr	Arg	Asp	Ile	Glu	Leu	Ile	Ser	Trp	Phe	Val	Ala	Ala
				85					90					95	
Gln	Phe	Leu	Leu	Asp	Thr	Thr	Leu	Glu	Ser	Ala	Ala	Asn	Ser	Leu	Glu
		100						105						110	

Trp Leu Ala Asp Leu Ser Glu Lys His Trp Asp His Leu Asn Pro Val
 115 120 125
 Leu Pro Val Glu Thr Leu Lys Ser Asp Asp Asp Lys Gly Lys Glu Arg
 130 135 140
 Glu Gln Ala Asp Ala Lys Val Lys Ala Phe Phe Gln Leu Val Gly Asp
 145 150 155 160
 Ser Glu Glu Ser Ser Ile Leu Tyr Ala Pro Val Leu Gln Leu Pro Leu
 165 170 175
 Val Gly Glu Val Thr Phe Phe Asp Phe Gln Ser Ala Glu Arg Lys Gly
 180 185 190
 Glu Ile Ser Gln Leu Lys Ser Met Leu Thr Thr Thr Val Ala Gln Glu
 195 200 205
 Arg Phe Ala Ile Gln Phe Lys Met Glu Asn Ala Lys Arg Cys Val Thr
 210 215 220
 Gln Leu Asp Arg Leu Ser Ala Leu Val Ser Thr Lys Cys His Ser Leu
 225 230 235 240
 Gly Ser Gln Ser Thr Asn Phe Gly Phe Ala Lys Ser Leu Leu Thr Arg
 245 250 255
 Val Glu Asn Ala Leu Val His Leu Ser Gly Ile Lys Leu Ala Pro Lys
 260 265 270
 Ala Glu Ala Lys Thr Val Glu Gln Glu Val Ala Glu Ser Ser Val Ser
 275 280 285
 Glu Gly Glu Leu Pro Ser His Met Asp Thr Lys His Ile Glu Arg Ile
 290 295 300
 Pro Met Ala Ser Glu Gln Ala Gln Thr Val Ser Gln His Leu His Ala
 305 310 315 320
 Gly Asn Leu Ser Glu Leu Gly Asn Leu Asn Asn Met Asn Arg Asp Leu
 325 330 335
 Ala Phe His Leu Leu Arg Glu Val Ser Asp Tyr Phe Arg Gln Ser Glu
 340 345 350
 Pro His Ser Pro Ile Ser Phe Leu Leu Glu Lys Ala Ile Arg Trp Gly
 355 360 365
 Tyr Leu Ser Leu Pro Glu Leu Leu Arg Glu Met Met Ser Glu Gln Asn
 370 375 380
 Gly Asp Ala Leu Ser Thr Ile Phe Asn Ala Ala Gly Leu Asn His Leu
 385 390 395 400
 Asp Gln Val Leu Leu Pro Glu Val Ser Thr Pro Thr Val Gly Ile Glu
 405 410 415

Ser Pro Gln Thr Pro Gln Ala Lys Pro Ser Val Ser Asp Pro Arg Ser
 420 425 430

Val Glu Glu His Val Ser Gln Thr Ser Pro Val Asp Thr Gln Ser Lys
 435 440 445

Gln Asp Gln Lys Pro Gln Ser Ser Ala Thr Ser Ala Leu Ser Trp
 450 455 460

<210> 3

<211> 176

<212> PRT

<213> V. Anguillarum

<400> 3

Met Ala Ser Ile Tyr Met Arg Val Ser Gly Leu Gln Val Glu Gly Ala
 1 5 10 15

Ala Thr Ile Gly Gln Leu Glu Thr Ala Glu Gly Lys Asn Asp Gly Trp
 20 25 30

Phe Ala Ile Asn Ser Tyr Ser Trp Gly Gly Ala Arg Asn Val Ala Met
 35 40 45

Asp Ile Gly Asn Gly Thr Asn Ala Asp Ser Gly Met Val Gly Val Ser
 50 55 60

Glu Val Ser Val Thr Lys Glu Val Asp Gly Ala Ser Glu Asp Leu Leu
 65 70 75 80

Ser Tyr Leu Phe Asn Pro Gly Lys Asp Gly Lys Thr Val Glu Val Ala
 85 90 95

Phe Thr Lys Pro Ser Asn Asp Gly Gln Gly Ala Asp Val Tyr Phe Gln
 100 105 110

Val Lys Leu Glu Lys Ala Arg Leu Val Ser Tyr Asn Val Ser Gly Thr
 115 120 125

Asp Gly Ser Gln Pro Tyr Glu Ser Leu Ser Leu Ser Tyr Thr Ser Ile
 130 135 140

Ser Gln Lys His His Tyr Glu Lys Glu Gly Gly Glu Leu Gln Ser Gly
 145 150 155 160

Gly Val Val Thr Tyr Asp Leu Pro Thr Gly Lys Met Thr Ser Gly Lys
 165 170 175

<210> 4

<211> 117

<212> PRT

<213> V. Anguillarum

<220>

<223> "Xaa" may be any, other or unknown amino acid

<400> 4

Met Ala Leu Asn Ser Gln His Lys Arg Val Ser Lys Asn Arg Val Ser
 1 5 10 15

Ile Thr Tyr Asp Val Glu Thr Asn Gly Ala Val Lys Thr Lys Glu Leu
 20 25 30

Pro Phe Val Val Gly Val Ile Gly Asp Phe Ser Gly His Lys Pro Glu
 35 40 45

Ser Glu Lys Val Asp Leu Glu Glu Arg Glu Phe Thr Gly Ile Asp Lys
 50 55 60

Asp Asn Phe Asp Thr Val Met Gly Gln Ile His Pro Arg Leu Ser Tyr
 65 70 75 80

Lys Val Asp Asn Lys Leu Ala Asn Asp Asp Ser Gln Phe Glu Val Asn
 85 90 95

Leu Ser Leu Arg Ser Met Lys Asp Phe His Pro Glu Asn Leu Val Asp
 100 105 110

Xaa Ile Glu Pro Leu
 115